

#4

0502 07/04 0300



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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/037,270

DATE: 01/22/2002

TIME: 14:28:38

Input Set : D:\pt_FL.784CIP2B.071000.fix
 Output Set: N:\CRF3\01182002\J037270.raw

4 <110> APPLICANT: Tang, Y. Tom
 5 Liu, Chenghua
 6 Asundi, Vinod
 7 Zhang, Jie
 8 Ren, Feiyan
 9 Chen, Rui-hong
 10 Zhao, Qing A.
 11 Wehrman, Tom
 12 Xue, Aidong J.
 13 Yang, Yonghong
 14 Wang, Jian-Rui
 15 Zhou, Ping
 16 Ma, Yunqing
 17 Wang, Dunrui
 18 Wang, Zhiwei
 19 Tillinghast, John
 20 Drmanac, Radoje T.
 23 <120> TITLE OF INVENTION: Novel Nucleic Acids and
 24 Polypeptides
 28 <130> FILE REFERENCE: 784CIP2B
 C--> 30 <140> CURRENT APPLICATION NUMBER: US/10/037,270
 C--> 31 <141> CURRENT FILING DATE: 2002-01-04
 33 <150> PRIOR APPLICATION NUMBER: 09/552,317
 34 <151> PRIOR FILING DATE: 2000-04-25
 36 <150> PRIOR APPLICATION NUMBER: 09/488,725
 37 <151> PRIOR FILING DATE: 2000-01-21
 40 <160> NUMBER OF SEQ ID NOS: 1104
 42 <170> SOFTWARE: pt_FL_genes Version 1.0
 48 <210> SEQ ID NO: 1
 49 <211> LENGTH: 2063
 50 <212> TYPE: DNA
 51 <213> ORGANISM: Homo sapiens
 53 <220> FEATURE:
 54 <221> NAME/KEY: CDS
 55 <222> LOCATION: (1)..(1677)
 57 <400> SEQUENCE: 1
 58 atg agg ttc tcg ctg gac aag gac acg gga ctc atc atg ctg att gcc 48
 59 Met Arg Phe Ser Leu Asp Lys Asp Thr Gly Leu Ile Met Leu Ile Ala
 60 1 5 10 15
 62 agg ctg gac tat gag ctc atc cag cgc ttc acc ctg acg atc att gcc 96
 63 Arg Leu Asp Tyr Glu Leu Ile Gln Arg Phe Thr Leu Thr Ile Ile Ala
 64 20 25 30
 66 cgg gac ggg ggc gag gag acc aca ggc cgg gtc agg atc aat gtg 144

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67	Arg Asp Gly Gly Glu Glu Thr Thr Gly Arg Val Arg Ile Asn Val			
68	35	40	45	
70	ttg gat gtc aac gac aac gtg ccc acc ttc cag aag gat gcc tac gtg	192		
71	Leu Asp Val Asn Asp Asn Val Pro Thr Phe Gln Lys Asp Ala Tyr Val			
72	50	55	60	
74	ggt gct ctg cgg gag aac gag cct tct gtc aca cag ctg gtg cgg ctc	240		
75	Gly Ala Leu Arg Glu Asn Glu Pro Ser Val Thr Gln Leu Val Arg Leu			
76	65	70	75	80
78	cgg gca aca gat gaa gac tcc cct ccc aac aac cag atc acc tac agc	288		
79	Arg Ala Thr Asp Glu Asp Ser Pro Pro Asn Asn Gln Ile Thr Tyr Ser			
80	85	90	95	
82	att gtc agt gca tct gcc ttt ggc agc tac ttc gac atc agc ctg tac	336		
83	Ile Val Ser Ala Ser Ala Phe Gly Ser Tyr Phe Asp Ile Ser Leu Tyr			
84	100	105	110	
86	gag ggc tat gga gtg atc agc gtc agt cgc ccc ctg gat tat gaa cag	384		
87	Glu Gly Tyr Gly Val Ile Ser Val Ser Arg Pro Leu Asp Tyr Glu Gln			
88	115	120	125	
90	ata tcc aat ggg ctg att tat ctg acg gtc atg gcc atg gat gct ggc	432		
91	Ile Ser Asn Gly Leu Ile Tyr Leu Thr Val Met Ala Met Asp Ala Gly			
92	130	135	140	
94	aac ccc cct ctc aac agc acc gtc cct gtc acc atc gag gtg ttt gat	480		
95	Asn Pro Pro Leu Asn Ser Thr Val Pro Val Thr Ile Glu Val Phe Asp			
96	145	150	155	160
98	gag aat gac gac cct ccc acc ttc agc aag ccc gcc tac ttc gtc tcc	528		
99	Glu Asn Asp Asp Pro Pro Thr Phe Ser Lys Pro Ala Tyr Phe Val Ser			
100	165	170	175	
102	gtg gtg gag aac atc atg gca gga gcc acg gtg ctg ttc ctg aat gcc	576		
103	Val Val Glu Asn Ile Met Ala Gly Ala Thr Val Leu Phe Leu Asn Ala			
104	180	185	190	
106	aca gac ctg gac cgc tcc cgg gag tac ggc cag gag tcc atc atc tac	624		
107	Thr Asp Leu Asp Arg Ser Arg Glu Tyr Gly Gln Glu Ser Ile Ile Tyr			
108	195	200	205	
110	tcc ttg gaa ggc tcc acc cag ttt cgg atc aat gcc cgc tca ggg gaa	672		
111	Ser Leu Glu Gly Ser Thr Gln Phe Arg Ile Asn Ala Arg Ser Gly Glu			
112	210	215	220	
114	atc acc acc acg tct ctg ctt gac cga gag acc aag tct gaa tac atc	720		
115	Ile Thr Thr Ser Leu Leu Asp Arg Glu Thr Lys Ser Glu Tyr Ile			
116	225	230	235	240
118	ctc atc gtt cgc gca gtg gac ggg ggt gtg ggc cac aac cag aaa act	768		
119	Leu Ile Val Arg Ala Val Asp Gly Gly Val Gly His Asn Gln Lys Thr			
120	245	250	255	
122	ggc atc gcc acc gta aac atc acc ctc ctg gac atc aac gac aac cac	816		
123	Gly Ile Ala Thr Val Asn Ile Thr Leu Leu Asp Ile Asn Asp Asn His			
124	260	265	270	
126	ccc acg tgg aag gac gca ccc tac tac atc aac ctg gtg gag atg acc	864		
127	Pro Thr Trp Lys Asp Ala Pro Tyr Tyr Ile Asn Leu Val Glu Met Thr			
128	275	280	285	
130	cct cca gac tct gac gtg acc acg gtg gtg gct gtt gac cca gac ctg	912		
131	Pro Pro Asp Ser Asp Val Thr Val Val Ala Val Asp Pro Asp Leu			

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132	290	295	300	
134	ggg gag aat ggc acc ctg gtg tac agc atc cag cca ccc aac aag ttc			960
135	Gly Glu Asn Gly Thr Leu Val Tyr Ser Ile Gln Pro Pro Asn Lys Phe			
136	305	310	315	320
138	tac agc ctc aac agc acc acg ggc aag atc cgc acc acc cac gcc atg			1008
139	Tyr Ser Leu Asn Ser Thr Thr Gly Lys Ile Arg Thr Thr His Ala Met			
140	325	330	330	335
142	ctg gac cgg gag aac ccc gac ccc cat gag gcc gag ctg atg cgc aaa			1056
143	Leu Asp Arg Glu Asn Pro Asp Pro His Glu Ala Glu Leu Met Arg Lys			
144	340	345	350	
146	atc gtc gtc tct gtt act gac tgt ggc agg ccc cct ctg aaa gcc acc			1104
147	Ile Val Val Ser Val Thr Asp Cys Gly Arg Pro Pro Leu Lys Ala Thr			
148	355	360	365	
150	agc agt gcc aca gtg ttt gtg aac ctc ttg gat ctc aat gac aat gac			1152
151	Ser Ser Ala Thr Val Phe Val Asn Leu Leu Asp Leu Asn Asp Asn Asp			
152	370	375	380	
154	ccc acc ttt cag aac ctg cct ttt gtg gcc gag gtg ctt gaa ggc atc			1200
155	Pro Thr Phe Gln Asn Leu Pro Phe Val Ala Glu Val Leu Glu Gly Ile			
156	385	390	395	400
158	ccg gcg ggg gtc tcc atc tac caa gtg gtg gcc atc gac ctc gat gag			1248
159	Pro Ala Gly Val Ser Ile Tyr Gln Val Ala Ile Asp Leu Asp Glu			
160	405	410	415	
162	ggc ctg aac ggc ctg gtg tcc tac cgc atg ccg gtg ggc atg ccc cgc			1296
163	Gly Leu Asn Gly Leu Val Ser Tyr Arg Met Pro Val Gly Met Pro Arg			
164	420	425	430	
166	atg gac ttc ctc atc aac agc agc ggc gtg gtg gtc acc acc acc			1344
167	Met Asp Phe Leu Ile Asn Ser Ser Gly Val Val Val Thr Thr Thr			
168	435	440	445	
170	gag ctg gac cgc gag cgc atc gcg gag tac cag ctg cgg gtg gtg gcc			1392
171	Glu Leu Asp Arg Glu Arg Ile Ala Glu Tyr Gln Leu Arg Val Val Ala			
172	450	455	460	
174	agt gat gca ggc acg ccc acc aag agc tcc acc agc acg ctc acc atc			1440
175	Ser Asp Ala Gly Thr Pro Thr Lys Ser Ser Thr Ser Thr Leu Thr Ile			
176	465	470	475	480
178	cat gtg ctg gat gtg aac gac gag acg ccc acc ttc ttc ccg gcc gtg			1488
179	His Val Leu Asp Val Asn Asp Glu Thr Pro Thr Phe Phe Pro Ala Val			
180	485	490	495	
182	tac aat gtg tct gtg tcc gag gac gtg cca cgc gag ttc cgg gtg gtc			1536
183	Tyr Asn Val Ser Val Ser Glu Asp Val Pro Arg Glu Phe Arg Val Val			
184	500	505	510	
186	tgg ctg aac tgc acg gac aac gac gtg ggc ctc aat gca gag ctc agc			1584
187	Trp Leu Asn Cys Thr Asp Asn Asp Val Gly Leu Asn Ala Glu Leu Ser			
188	515	520	525	
190	tac ttc atc aca ggt gct gcc ccg gcc tcc acc cac ctg tgc agg cct			1632
191	Tyr Phe Ile Thr Gly Ala Ala Pro Ala Ser Thr His Leu Cys Arg Pro			
192	530	535	540	
194	cct ggg gcc ctg cct cca ccc ctc cca gat gga cag cca gac tag gtg			1680
195	Pro Gly Ala Leu Pro Pro Leu Pro Asp Gly Gln Pro Asp			
196	545	550	555	

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198 gggcaggtg agggtggaaa agaggtcagg gctctactgt tgggctttag cctctggtgg 1740
 200 tgcctccga ggatttgcgc ctggcttcc ccaaggcgtt tgcagctgga tcactctgga 1800
 202 ctggctccct gggacctcc tgaacctgtt ggtcaggg acggggagca tctaccaagg 1860
 204 ttcattctag agggaggtaa ggcccatga ttccctaggaa ggagccctga gccccactcc 1920
 206 ccccccagaag tctgggtgac agagcagtga cttggaggaa tgtggctca tccttccttg 1980
 208 gggacctgtt gagaattccc acctgtttag aggagatgg ttttgcgttc cctaaatgaa 2040
 210 atggtttttag ctcaaaaaaaa aaa 2063
 215 <210> SEQ ID NO: 2
 216 <211> LENGTH: 1352
 217 <212> TYPE: DNA
 218 <213> ORGANISM: Homo sapiens
 220 <220> FEATURE:
 221 <221> NAME/KEY: CDS
 222 <222> LOCATION: (209)..(673)
 224 <400> SEQUENCE: 2
 225 acaaccgttgccttttaag agaggcccg cccatccaga ggggggtgggg cagaggcgg 60
 227 gtctgaggag ctggggaaagg aacaaagcga ggccctgcggg cggcggctgg gctccggcgg 120
 229 ggccgcgggg tgccgggcct gcggcggcgg gcccggcgg agcgttggag ggaaggaggt 180
 231 ggcacatcgccg tccgcgcgg ccccgcc 10 atg aac ggg ctc ccc tcg gca gag 232
 232 Met Asn Gly Leu Pro Ser Ala Glu
 233 1 5
 235 gcg ccg ggc ggg gcg ggc tgc gct ttg gcc ggg ctc cca ccg ctg ccg 280
 236 Ala Pro Gly Gly Ala Gly Cys Ala Leu Ala Gly Leu Pro Pro Leu Pro 10 15 20
 237 10 15 20
 239 cgc ggc ctc agc ggc ctc ctt aat gcg agc ggg ggc tcg tgg cgg gag 328
 240 Arg Gly Leu Ser Gly Leu Leu Asn Ala Ser Gly Gly Ser Trp Arg Glu 25 30 35 40
 241 25 30 35 40
 243 ctg gag cgc gtc tac agc cag cgc agc cgc atc cac gac gag ctg agc 376
 244 Leu Glu Arg Val Tyr Ser Gln Arg Ser Arg Ile His Asp Glu Leu Ser 45 50 55
 245 45 50 55
 247 cgc gcc gcc cgc gcc ccc gac ggg ccc cgc cac gcc gcc ggc gcc gcc 424
 248 Arg Ala Ala Arg Ala Pro Asp Gly Pro Arg His Ala Ala Gly Ala Ala 60 65 70
 249 60 65 70
 251 aac gcg gga ccc gca gcc ggc ccc cgt cgt cct gtc aac ctc gac tca 472
 252 Asn Ala Gly Pro Ala Ala Gly Pro Arg Arg Pro Val Asn Leu Asp Ser 75 80 85
 253 75 80 85
 255 gcg ctg gcc gcg ctg cgc aag gag atg ttg tct gca ggt ggg gct gcg 520
 256 Ala Leu Ala Ala Leu Arg Lys Glu Met Leu Ser Ala Gly Gly Ala Ala 90 95 100
 257 90 95 100
 259 gca gtt gga cat gtc ctt gtt gtg cca gct gtg ggg cct gta cga gtc 568
 260 Ala Val Gly His Val Leu Val Val Pro Ala Val Gly Pro Val Arg Val 105 110 115 120
 261 105 110 115 120
 263 aat cca gga cta caa aca cct gtg cca aga cct gag ctt ctg cca gga 616
 264 Asn Pro Gly Leu Gln Thr Pro Val Pro Arg Pro Glu Leu Leu Pro Gly 125 130 135
 265 125 130 135
 267 cct gtc atc ctc cct cca ttc gga cag ctc cta ccc acc gga tgc ggg 664
 268 Pro Val Ile Leu Pro Pro Phe Gly Gln Leu Leu Pro Thr Gly Cys Gly 140 145 150
 269 140 145 150
 271 cct gtc tga cgacgag gagcctcccg atgccagct gcctcctgac cggccacccc 720

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272 Pro Val
 275 ttactgtgcc ccagacgcac aatgccgtg accagtggct gcaggatgcc ttccacatca 780
 277 gcctctgaag ggctgggggg cagggggcat gcacccatgc aaaaggctca gaaaactcccc 840
 279 ctccggcaag ccctcagact tcggagctg cgccttcccc cctaccgcct cacctcacag 900
 281 gagggccagg catgtattcc tcagaggcga aactgc当地 ctctttctcc tgtcttgggt 960
 283 tggctggcac tggggcgggc atctaggta cagcctctgc tcatggcact gggcctccag 1020
 285 ttcttcaca tgggtgcacc cccagcttgg ccaaccctca gccttgcggg ggggccccgaa 1080
 287 gcatctccc ttccgcttgg cgtctctggg attggatga gtgcctggct cccatctcct 1140
 289 cctcacctt tgggtctatc ggcagctgct ggctcagggg catcccaccc cccggctctg 1200
 291 gggtcctctg ccctggagg gctccaggac ccgtcccaat aaccacccac gggcaggagg 1260
 293 gccaaggccc cgtgctggat atttaattt agggccggg ctccagggcg cgtagataaaa 1320
 295 taaatacact cagcgtcaaa aaaaaaaaaa aa 1352
 300 <210> SEQ ID NO: 3
 301 <211> LENGTH: 5143
 302 <212> TYPE: DNA
 303 <213> ORGANISM: Homo sapiens
 305 <220> FEATURE:
 306 <221> NAME/KEY: CDS
 307 <222> LOCATION: (501)..(4277)
 309 <400> SEQUENCE: 3
 310 tgggtcttga gactcgatat acctatctat tcgatgtatg agataccca ccagacccaa 60
 312 aaaaagagat ctctcgagga tccgaattcg cggccgcgtc gaccgcgccc ctgcccggc 120
 314 ccctagctcg ggcctcaggg gcctccctt tccggcagg cccgtccctg cagcaaggca 180
 316 gtgagcaccc cggccagcag agggcgggtcc ggacccaaat ctgcagcggc gccattggcg 240
 318 tggaaaat gccaccagat ggccgggttag gattgcagct ccgttgaagg cggggcccc 300
 320 gctcccgaaac ccccgccgac caccggtaa caacccccc acatgggaa taacacaccg 360
 322 gagacttttggggaaact aggtcgatgg tcggcggcgc ccggatgggc agctgaggat 420
 324 tgcctttag gttattttaa aagtttttag ttgtacagca cttgattatt ttgtctgcatt 480
 326 gtgaaaggac ctctccagca atg att act tca gaa tta cca gtg tta cag 530
 327 Met Ile Thr Ser Glu Leu Pro Val Leu Gln
 328 1 5 10
 330 gat tca act aat gaa act act gcc cat tcc gat gct ggc agc gag ctt 578
 331 Asp Ser Thr Asn Glu Thr Thr Ala His Ser Asp Ala Gly Ser Glu Leu
 332 15 20 25
 334 gaa gaa aca gag gtc aaa gga aaa aga aaa agg ggt cgt cct ggc cgg 626
 335 Glu Glu Thr Glu Val Lys Gly Lys Arg Lys Arg Gly Arg Pro Gly Arg
 336 30 35 40
 338 cct cca tct aca aat aag aaa cct cga aaa tct cca ggt gag aag agc 674
 339 Pro Pro Ser Thr Asn Lys Lys Pro Arg Lys Ser Pro Gly Glu Lys Ser
 340 45 50 55
 342 aga att gaa gct gga att aga gga gca ggc cgt gga aga gct aat gga 722
 343 Arg Ile Glu Ala Gly Ile Arg Gly Ala Gly Arg Gly Arg Ala Asn Gly
 344 60 65 70
 346 cac cct caa cag aat ggg gaa ggg gag cct gtc aca tta ttt gag gtg 770
 347 His Pro Gln Gln Asn Gly Glu Gly Glu Pro Val Thr Leu Phe Glu Val
 348 75 80 85 90
 350 gtg aaa ctg ggg aaa agt gca atg cag tcc gtg gtg gat gac tgg att 818
 351 Val Lys Leu Gly Lys Ser Ala Met Gln Ser Val Val Asp Asp Trp Ile
 352 95 100 105

Use of n and/or Xaa has been detected in the Sequence Listing.
 → Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY
 PATENT APPLICATION: US/10/037,270

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Input Set : D:\pt_FL.784CIP2B.071000.fix
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L:30 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:31 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:1568 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
 L:1570 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
 L:1780 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
 L:1784 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
 L:2008 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
 L:2012 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
 L:2206 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
 L:7920 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
 L:8681 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52
 L:8845 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
 L:11343 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65
 L:11717 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
 L:11719 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
 L:11721 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
 L:12082 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68
 L:12979 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73
 L:21539 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:110
 L:21541 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:110
 L:29074 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:144
 L:31963 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:156
 L:31967 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:156
 L:31969 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:156
 L:33650 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:165
 L:35021 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174
 L:36554 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:183
 L:37368 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:188
 L:37428 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:188
 L:37430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:188
 L:37432 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:188
 L:40315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:206
 L:40411 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:206
 L:40413 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:206
 L:46364 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:242
 L:52411 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:263
 L:54132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:270
 L:55761 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:279
 L:58873 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:293
 L:59157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:294
 L:59511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:295
 L:59513 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:295
 L:61314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:303
 L:67002 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:330
 L:67004 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:330
 L:68053 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:332
 L:74607 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:356
 L:74609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:356

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Input Set : D:\pt_FL.784CIP2B.071000.fix
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L:74833 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:357

L:74835 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:357

L:74855 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:358

L:76524 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:367